



SEQUENCE LISTING

<110> BATEMAN, JOHN
FITZGERALD, DAVID

<120> A MOLECULAR MARKER

<130> 071838.0142

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<150> PCT/AU02/00542

<151> 2002-05-02

<150> AU PR4701/01

<151> 2001-05-02

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<170> PatentIn Ver. 3.3

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<210> 20

<211> 418

<212> PRT

<213> Homo sapiens

<400> 20

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Met Leu Pro Trp Thr Ala Leu Gly Leu Ala Leu Ser Leu Arg Leu Ala
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Leu Ala Arg Ser Gly Ala Glu Arg Gly Pro Pro Ala Ser Ala Pro Arg
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Gly Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr
          35           40           45

Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu
          50           55           60

Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser
          65           70           75           80

Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala
          85           90           95

Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr His
          100          105          110

Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala
          115          120          125

Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp
          130          135          140

Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp
          145          150          155          160

Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu
          165          170          175

Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe
          180          185          190

Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser
          195          200          205

Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr
          210          215          220

Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser
          225          230          235          240

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Glu Pro

<400> 21

Met	Leu	Phe	Trp	Thr	Ala	Phe	Ser	Met	Ala	Leu	Ser	Leu	Arg	Leu	Ala
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Leu	Ala	Arg	Ser	Ser	Ile	Glu	Arg	Gly	Ser	Thr	Ala	Ser	Asp	Pro	Gln
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Gly	Asp	Leu	Leu	Phe	Leu	Leu	Asp	Ser	Ser	Ala	Ser	Val	Ser	His	Tyr
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Glu	Phe	Ser	Arg	Val	Arg	Glu	Phe	Val	Gly	Gln	Leu	Val	Ala	Thr	Met
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Ser	Phe	Gly	Pro	Gly	Ala	Leu	Arg	Ala	Ser	Leu	Val	His	Val	Gly	Ser
65					70					75					80

Gln	Pro	His	Thr	Glu	Phe	Thr	Phe	Asp	Gln	Tyr	Ser	Ser	Gly	Gln	Ala	
				85					90					95		
Ile	Arg	Asp	Ala	Ile	Arg	Val	Ala	Pro	Gln	Arg	Met	Gly	Asp	Thr	Asn	
			100					105					110			
Thr	Gly	Leu	Ala	Leu	Ala	Tyr	Ala	Lys	Glu	Gln	Leu	Phe	Ala	Glu	Glu	
		115					120					125				
Ala	Gly	Ala	Arg	Pro	Gly	Val	Pro	Lys	Val	Leu	Val	Trp	Val	Thr	Asp	
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Gly	Gly	Ser	Ser	Asp	Pro	Val	Gly	Pro	Pro	Met	Gln	Glu	Leu	Lys	Asp	
145					150					155					160	
Leu	Gly	Val	Thr	Ile	Phe	Ile	Val	Ser	Thr	Gly	Arg	Gly	Asn	Leu	Leu	
				165					170					175		
Glu	Leu	Leu	Ala	Ala	Ala	Ser	Ala	Pro	Ala	Glu	Lys	His	Leu	His	Phe	
			180					185					190			
Val	Asp	Val	Asp	Asp	Leu	Pro	Ile	Ile	Ala	Arg	Glu	Leu	Arg	Gly	Ser	
		195					200					205				
Ile	Thr	Asp	Ala	Met	Gln	Pro	Gln	Gln	Leu	His	Ala	Ser	Glu	Val	Leu	
	210					215					220					
Ser	Ser	Gly	Phe	Arg	Leu	Ser	Trp	Pro	Pro	Leu	Leu	Thr	Ala	Asp	Ser	
225					230					235					240	
Gly	Tyr	Tyr	Val	Leu	Glu	Leu	Val	Pro	Ser	Gly	Lys	Leu	Ala	Thr	Thr	
			245						250					255		
Arg	Arg	Gln	Gln	Leu	Pro	Gly	Asn	Ala	Thr	Ser	Trp	Thr	Trp	Thr	Asp	
			260					265					270			
Leu	Asp	Pro	Asp	Thr	Asp	Tyr	Glu	Val	Ser	Leu	Leu	Pro	Glu	Ser	Asn	
		275					280					285				
Val	His	Leu	Leu	Arg	Pro	Gln	His	Val	Arg	Val	Arg	Thr	Leu	Gln	Glu	
	290					295					300					
Glu	Ala	Gly	Pro	Glu	Arg	Ile	Val	Ile	Ser	His	Ala	Arg	Pro	Arg	Ser	
305					310					315					320	
Leu	Arg	Val	Ser	Trp	Ala	Pro	Ala	Leu	Gly	Pro	Asp	Ser	Ala	Leu	Gly	
			325						330					335		
Tyr	His	Val	Gln	Leu	Gly	Pro	Leu	Gln	Gly	Gly	Ser	Leu	Glu	Arg	Val	
			340					345					350			
Glu	Val	Pro	Ala	Gly	Gln	Asn	Ser	Thr	Thr	Val	Gln	Gly	Leu	Thr	Pro	
		355					360					365				
Cys	Thr	Thr	Tyr	Leu	Val	Thr	Val	Thr	Ala	Ala	Phe	Arg	Ser	Gly	Arg	
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Gln Arg Ala Leu Ser Ala Lys Ala Cys Thr Ala Ser Gly Ala Arg Thr
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Arg Ala Pro Gln Ser Met Arg Pro Glu Ala Gly Pro Arg Glu Pro
 405 410 415

<210> 22

<211> 182

<212> PRT

<213> Gullus gallus

<400> 22

Ile Ala Asp Ile Val Ile Leu Val Asp Gly Ser Trp Ser Ile Gly Arg
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Phe Asn Phe Arg Leu Val Arg Leu Phe Leu Glu Asn Leu Val Ser Ala
 20 25 30

Phe Asn Val Gly Ser Glu Lys Thr Arg Val Gly Leu Ala Gln Tyr Ser
 35 40 45

Gly Asp Pro Arg Ile Glu Trp His Leu Asn Ala Tyr Gly Thr Lys Asp
 50 55 60

Ala Val Leu Asp Ala Val Arg Asn Leu Pro Tyr Lys Gly Gly Asn Thr
 65 70 75 80

Leu Thr Gly Leu Ala Leu Thr Tyr Ile Leu Glu Asn Ser Phe Lys Pro
 85 90 95

Glu Ala Gly Ala Arg Pro Gly Val Ser Lys Ile Gly Ile Leu Ile Thr
 100 105 110

Asp Gly Lys Ser Gln Asp Asp Val Ile Pro Pro Ala Lys Asn Leu Arg
 115 120 125

Asp Ala Gly Ile Glu Leu Phe Ala Ile Gly Val Lys Asn Ala Asp Ile
 130 135 140

Asn Glu Leu Lys Glu Ile Ala Ser Glu Pro Asp Ser Thr His Val Tyr
 145 150 155 160

Asn Val Ala Asp Phe Asn Phe Met Asn Ser Ile Val Glu Gly Leu Thr
 165 170 175

Arg Thr Val Cys Ser Arg
 180

<210> 23

<211> 183

<212> PRT

<213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: VA domain from
 Unknown collagen VII

<400> 23

Ala Ala Asp Ile Val Phe Leu Leu Asp Gly Ser Ser Ser Ile Gly Arg
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Ser Asn Phe Arg Glu Val Arg Ser Phe Leu Glu Gly Leu Val Leu Pro
 20 25 30

Phe Ser Gly Ala Ala Ser Ala Gln Gly Val Arg Phe Ala Thr Val Gln
 35 40 45

Tyr Ser Asp Asp Pro Arg Thr Glu Phe Gly Leu Asp Ala Leu Gly Ser
 50 55 60

Gly Gly Asp Val Ile Arg Ala Ile Arg Glu Leu Ser Tyr Lys Gly Gly
 65 70 75 80

Asn Thr Arg Thr Gly Ala Ala Ile Leu His Val Ala Asp His Val Phe
 85 90 95

Leu Pro Gln Leu Ala Arg Pro Gly Val Pro Lys Val Cys Ile Leu Ile
 100 105 110

Thr Asp Gly Lys Ser Gln Asp Leu Val Asp Thr Ala Ala Gln Arg Leu
 115 120 125

Lys Gly Gln Gly Val Lys Leu Phe Ala Val Gly Ile Lys Asn Ala Asp
 130 135 140

Pro Glu Glu Leu Lys Arg Val Ala Ser Gln Pro Thr Ser Asp Phe Phe
 145 150 155 160

Phe Phe Val Asn Asp Phe Ser Ile Leu Arg Thr Leu Leu Pro Leu Val
 165 170 175

Ser Arg Arg Val Cys Thr Thr
 180

<210> 24

<211> 182

<212> PRT

<213> Homo sapiens

<400> 24

Lys Ala Asp Ile Val Phe Leu Thr Asp Ala Ser Trp Ser Ile Gly Asp
 1 5 10 15

Asp Asn Phe Asn Lys Val Val Lys Phe Ile Phe Asn Thr Val Gly Ala
 20 25 30

Phe Asp Glu Val Asn Pro Ala Gly Ile Gln Val Ser Phe Val Gln Tyr
 35 40 45

Ser Asp Glu Val Lys Ser Glu Phe Lys Leu Asn Thr Tyr Asn Asp Lys
 50 55 60

Ala Leu Ala Leu Gly Ala Leu Gln Asn Ile Arg Tyr Arg Gly Gly Asn
65 70 75 80

Thr Arg Thr Gly Lys Ala Leu Thr Phe Ile Lys Glu Lys Val Leu Thr
85 90 95

Trp Glu Ser Gly Met Arg Lys Asn Val Arg Val Leu Gly Val Val Thr
100 105 110

Asp Gly Arg Ser Gln Asp Glu Val Lys Lys Ala Ala Phe Val Ile Gln
115 120 125

Gln Ser Gly Phe Ser Val Phe Val Val Gly Val Ala Asp Val Asp Tyr
130 135 140

Asn Glu Leu Ala Asn Ile Ala Ser Lys Pro Ser Glu Arg His Val Phe
145 150 155 160

Ile Val Asp Asp Phe Glu Ser Phe Glu Lys Ile Glu Asp Asn Leu Ile
165 170 175

Thr Phe Val Cys Glu Thr
180

<210> 25
<211> 185
<212> PRT
<213> Unknown Sequence

<220>
<223> Description of Unknown Sequence: VA domain from
Unknown collagen VI

<400> 25
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Asp Arg Phe Leu Leu Val Gln Glu Phe Leu Ser Asp Val Val Glu Ser
20 25 30

Leu Ala Val Gly Asp Asn Asp Phe His Phe Ala Leu Val Arg Leu Asn
35 40 45

Gly Asn Pro His Thr Glu Phe Leu Leu Asn Thr Tyr His Ser Lys Gln
50 55 60

Glu Val Leu Ser His Ile Ala Asn Met Ser Tyr Ile Gly Gly Ser Asn
65 70 75 80

Gln Thr Gly Lys Gly Leu Glu Tyr Val Ile His Ser His Leu Thr Glu
85 90 95

Ala Ser Gly Ser Arg Ala Ala Asp Gly Val Pro Gln Val Ile Val Val
100 105 110

Leu Thr Asp Gly Gln Ser Glu Asp Gly Phe Ala Leu Pro Ser Ala Glu
115 120 125

Leu Lys Ser Ala Asp Val Asn Val Phe Ala Val Gly Val Glu Gly Ala
 130 135 140
 Asp Glu Arg Ala Leu Gly Glu Val Ala Ser Glu Pro Leu Leu Ser Met
 145 150 155 160
 His Val Phe Asn Leu Glu Asn Val Thr Ser Leu His Gly Leu Val Gly
 165 170 175
 Asn Leu Val Ser Cys Ile His Ser Ser
 180 185

<210> 26
 <211> 185
 <212> PRT
 <213> Mus musculus

<400> 26
 Arg Ala Asp Leu Val Phe Ile Ile Asp Ser Ser Arg Ser Val Asn Thr
 1 5 10 15
 Tyr Asp Tyr Ala Lys Val Lys Glu Phe Ile Leu Asp Ile Leu Gln Phe
 20 25 30
 Leu Asp Ile Gly Pro Asp Val Thr Arg Val Gly Leu Leu Gln Tyr Gly
 35 40 45
 Ser Thr Val Lys Asn Glu Phe Ser Leu Lys Thr Phe Lys Arg Lys Ser
 50 55 60
 Glu Val Glu Arg Ala Val Lys Arg Met Arg His Leu Ser Thr Gly Thr
 65 70 75 80
 Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu Asn Ile Ala Phe Ser Glu
 85 90 95
 Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn Val Pro Arg Ile Ile Met
 100 105 110
 Ile Val Thr Asp Gly Arg Pro Gln Asp Ser Val Ala Glu Val Ala Ala
 115 120 125
 Lys Ala Arg Asn Thr Gly Ile Leu Ile Phe Ala Ile Gly Val Gly Gln
 130 135 140
 Val Asp Leu Asn Thr Leu Lys Ala Ile Gly Ser Glu Pro His Lys Asp
 145 150 155 160
 His Val Phe Leu Val Ala Asn Phe Ser Gln Ile Glu Ser Leu Thr Ser
 165 170 175
 Val Phe Gln Asn Lys Leu Cys Thr Val
 180 185

<210> 27
 <211> 184
 <212> PRT
 <213> Mus musculus

<400> 27
 Pro Leu Asp Leu Val Phe Met Ile Asp Ser Ser Arg Ser Val Arg Pro
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 Phe Glu Phe Glu Thr Met Arg Gln Phe Leu Val Gly Leu Leu Arg Ser
 20 25 30
 Leu Asp Val Gly Leu Asn Ala Thr Arg Val Gly Val Ile Gln Tyr Ser
 35 40 45
 Ser Gln Val Gln Ser Val Phe Pro Leu Gly Ala Phe Ser Arg Arg Glu
 50 55 60
 Asp Met Glu Arg Ala Ile Arg Ala Val Val Pro Leu Ala Gln Gly Thr
 65 70 75 80
 Met Thr Gly Leu Ala Ile Gln Tyr Ala Met Asn Val Ala Phe Ser Glu
 85 90 95
 Ala Glu Gly Ala Arg Pro Ser Glu Glu Arg Val Pro Arg Val Leu Val
 100 105 110
 Ile Val Thr Asp Gly Arg Pro Gln Asp Arg Val Ala Glu Val Ala Ala
 115 120 125
 Gln Ala Arg Ala Arg Gly Ile Glu Ile Tyr Ala Val Gly Val Gln Arg
 130 135 140
 Ala Asp Val Gly Ser Leu Arg Thr Met Ala Ser Pro Pro Leu Asp Gln
 145 150 155 160
 His Val Phe Leu Val Glu Ser Phe Asp Ile Gln Glu Phe Gly Leu Gln
 165 170 175
 Phe Gln Gly Arg Leu Cys Gly Lys
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<210> 28
 <211> 185
 <212> PRT
 <213> Mus musculus

<400> 28
 Pro Leu Asp Leu Val Phe Ile Ile Asp Ser Ser Arg Ser Val Arg Pro
 1 5 10 15
 Leu Glu Phe Thr Lys Val Lys Thr Phe Val Ser Arg Ile Ile Asp Thr
 20 25 30
 Leu Asp Ile Gly Ala Thr Asp Thr Arg Val Ala Val Val Asn Tyr Ala
 35 40 45

Ser Thr Val Lys Ile Glu Phe Gln Leu Asn Thr Tyr Ser Asp Lys Gln
 50 55 60
 Ala Leu Lys Gln Ala Val Ala Arg Ile Thr Pro Leu Ser Thr Gly Thr
 65 70 75 80
 Met Ser Gly Leu Ala Ile Gln Thr Ala Met Glu Glu Ala Phe Thr Val
 85 90 95
 Glu Ala Gly Ala Arg Gly Pro Met Ser Asn Ile Pro Lys Val Ala Ile
 100 105 110
 Ile Val Thr Asp Gly Arg Pro Gln Asp Gln Val Asn Glu Val Ala Ala
 115 120 125
 Arg Ala Arg Ala Ser Gly Ile Glu Leu Tyr Ala Val Gly Val Asp Arg
 130 135 140
 Ala Asp Met Glu Ser Leu Lys Met Met Ala Ser Lys Pro Leu Glu Glu
 145 150 155 160
 His Val Phe Tyr Val Glu Thr Tyr Gly Val Ile Glu Lys Leu Ser Ala
 165 170 175
 Arg Phe Gln Glu Thr Pro Cys Ala Leu
 180 185

<210> 29
 <211> 185
 <212> PRT
 <213> Mus musculus

<400> 29
 Pro Thr Asp Leu Val Phe Val Val Asp Ser Ser Arg Ser Val Arg Pro
 1 5 10 15
 Val Glu Phe Glu Lys Val Lys Val Phe Leu Ser Gln Val Ile Glu Ser
 20 25 30
 Leu Asp Val Gly Pro Asn Ala Thr Arg Val Gly Leu Val Asn Tyr Ala
 35 40 45
 Ser Thr Val Lys Pro Glu Phe Pro Leu Arg Ala His Gly Ser Lys Ala
 50 55 60
 Ser Leu Leu Gln Ala Val Arg Arg Ile Gln Pro Leu Ser Thr Gly Thr
 65 70 75 80
 Met Thr Gly Leu Ala Leu Gln Phe Ala Ile Thr Lys Ala Leu Ser Asp
 85 90 95
 Ala Glu Gly Gly Arg Ala Arg Ser Pro Asp Ile Ser Lys Val Val Ile
 100 105 110
 Val Val Thr Asp Gly Arg Pro Gln Asp Ser Val Arg Asp Val Ser Glu
 115 120 125

Arg Ala Arg Ala Ser Gly Ile Glu Leu Phe Ala Ile Gly Leu Gly Arg
 130 135 140

Val Asp Lys Ala Thr Leu Arg Gln Ile Ala Ser Glu Pro Gln Asp Glu
 145 150 155 160

His Val Asp Tyr Val Glu Ser Tyr Asn Val Ile Glu Lys Leu Ala Lys
 165 170 175

Lys Phe Gln Glu Ala Phe Cys Val Val
 180 185

<210> 30
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 30
 Gln Leu Asp Ile Val Ile Val Leu Asp Gly Ser Asn Ser Ile Tyr Pro
 1 5 10 15

Trp Asp Ser Val Thr Ala Phe Leu Asn Asp Leu Leu Lys Arg Met Asp
 20 25 30

Ile Gly Pro Lys Gln Thr Gln Val Gly Ile Val Gln Tyr Gly Glu Asn
 35 40 45

Val Thr His Glu Phe Asn Leu Asn Lys Tyr Ser Ser Thr Glu Glu Val
 50 55 60

Leu Val Ala Ala Lys Lys Ile Val Gln Arg Gly Gly Arg Gln Thr Met
 65 70 75 80

Thr Ala Leu Gly Thr Asp Thr Ala Arg Lys Glu Ala Phe Thr Glu Ala
 85 90 95

Arg Gly Ala Arg Arg Gly Val Lys Lys Val Met Val Ile Val Thr Asp
 100 105 110

Gly Glu Ser His Asp Asn His Arg Leu Lys Lys Val Ile Gln Asp Cys
 115 120 125

Glu Asp Glu Asn Ile Gln Arg Phe Ser Ile Ala Ile Leu Gly Ser Tyr
 130 135 140

Asn Arg Gly Asn Leu Ser Thr Glu Lys Phe Val Glu Glu Ile Lys Ser
 145 150 155 160

Ile Ala Ser Glu Pro Thr Glu Lys His Phe Phe Asn Val Ser Asp Glu
 165 170 175

Leu Ala Leu Val Thr Ile Val Lys Thr Leu Gly Glu Arg Ile Phe Ala
 180 185 190

Leu

<210> 31
 <211> 181
 <212> PRT
 <213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: VA domain from
 Unknown WARP

<400> 31

Gln	Gly	Asp	Leu	Leu	Phe	Leu	Leu	Asp	Ser	Ser	Ala	Ser	Val	Ser	His	1	5	10	15
Tyr	Glu	Phe	Ser	Arg	Val	Arg	Glu	Phe	Val	Gly	Gln	Leu	Val	Ala	Thr	20	25	30	
Met	Ser	Phe	Gly	Pro	Gly	Ala	Leu	Arg	Ala	Ser	Leu	Val	His	Val	Gly	35	40	45	
Ser	Gln	Pro	His	Thr	Glu	Phe	Thr	Phe	Asp	Gln	Tyr	Ser	Ser	Gly	Gln	50	55	60	
Ala	Ile	Arg	Asp	Ala	Ile	Arg	Val	Ala	Pro	Gln	Arg	Met	Gly	Asp	Thr	65	70	75	80
Asn	Thr	Gly	Leu	Ala	Leu	Ala	Tyr	Ala	Lys	Glu	Gln	Leu	Phe	Ala	Glu	85	90	95	
Glu	Ala	Gly	Ala	Arg	Pro	Gly	Val	Pro	Lys	Val	Leu	Val	Trp	Val	Thr	100	105	110	
Asp	Gly	Gly	Ser	Ser	Asp	Pro	Val	Gly	Pro	Pro	Met	Gln	Glu	Leu	Lys	115	120	125	
Asp	Leu	Gly	Val	Thr	Ile	Phe	Ile	Val	Ser	Thr	Gly	Arg	Gly	Asn	Leu	130	135	140	
Leu	Glu	Leu	Leu	Ala	Ala	Ala	Ser	Ala	Pro	Ala	Glu	Lys	His	Leu	His	145	150	155	160
Phe	Val	Asp	Val	Asp	Asp	Leu	Pro	Ile	Ile	Ala	Arg	Glu	Leu	Arg	Gly	165	170	175	
Ser	Ile	Thr	Asp	Ala												180			

<210> 32
 <211> 184
 <212> PRT
 <213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: VA domain from
 Unknown cochlin

<400> 32

Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Tyr Asn Ile Gly Gln
 1 5 10 15
 Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala Val Met
 20 25 30
 Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Val Val Gln Ala Ser
 35 40 45
 Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ala Ala Lys
 50 55 60
 Glu Val Leu Phe Ala Ile Lys Glu Leu Gly Phe Arg Gly Gly Asn Ser
 65 70 75 80
 Asn Thr Gly Lys Ala Leu Lys His Ala Ala Gln Lys Phe Phe Ser Met
 85 90 95
 Glu Asn Gly Ala Arg Lys Gly Ile Pro Lys Ile Ile Val Val Phe Leu
 100 105 110
 Asp Gly Trp Pro Ser Asp Asp Leu Glu Glu Ala Gly Ile Val Ala Arg
 115 120 125
 Glu Phe Gly Val Asn Val Phe Ile Val Ser Ser Val Ala Lys Pro Thr
 130 135 140
 Thr Glu Glu Leu Gly Met Val Gln Asp Ile Gly Phe Ile Asp Lys Ala
 145 150 155 160
 Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr Gln Met Pro Ser Trp Phe
 165 170 175
 Gly Thr Thr Lys Tyr Val Lys Pro
 180

<210> 33

<211> 186

<212> PRT

<213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: VA domain from
 Unknown vwf

<400> 33

Leu Leu Asp Leu Val Phe Leu Leu Asp Gly Ser Ser Arg Leu Ser Glu
 1 5 10 15
 Ala Glu Phe Glu Val Leu Lys Ala Phe Val Val Asp Met Met Glu Arg
 20 25 30
 Leu Arg Ile Ser Gln Lys Trp Val Arg Val Ala Val Val Glu Tyr His
 35 40 45

Asp Gly Ser His Ala Tyr Ile Gly Leu Lys Asp Arg Lys Arg Pro Ser
 50 55 60
 Glu Leu Arg Arg Ile Ala Ser Gln Val Lys Tyr Ala Gly Ser Gln Val
 65 70 75 80
 Ala Ser Thr Ser Glu Val Leu Lys Tyr Thr Leu Phe Gln Ile Phe Ser
 85 90 95
 Lys Ile Asp Arg Pro Glu Ala Ser Arg Ile Ala Leu Leu Leu Met Ala
 100 105 110
 Ser Gln Glu Pro Gln Arg Met Ser Arg Asn Phe Val Arg Tyr Val Gln
 115 120 125
 Gly Leu Lys Lys Lys Lys Val Ile Val Ile Pro Val Gly Ile Gly Pro
 130 135 140
 His Ala Asn Leu Lys Gln Ile Arg Leu Ile Glu Lys Gln Ala Pro Glu
 145 150 155 160
 Asn Lys Ala Phe Val Leu Ser Ser Val Asp Glu Leu Glu Gln Gln Arg
 165 170 175
 Asp Glu Ile Val Ser Tyr Leu Cys Asp Leu
 180 185

<210> 34
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 34
 Pro Arg Asn Leu Lys Val Thr Asp Glu Thr Thr Asp Ser Phe Lys Ile
 1 5 10 15
 Thr Trp Thr Gln Ala Pro Gly Arg Val Leu Arg Tyr Arg Ile Ile Tyr
 20 25 30
 Arg Pro Val Ala Gly Gly Glu Ser Arg Glu Val Thr Thr Pro Pro Asn
 35 40 45
 Gln Arg Arg Arg Thr Leu Glu Asn Leu Ile Pro Asp Thr Lys Tyr Glu
 50 55 60
 Val Ser Val Ile Pro Glu Tyr Phe Ser Gly Pro Gly Thr Pro Leu Thr
 65 70 75 80
 Gly Asn Ala Ala Thr
 85

<210> 35
 <211> 86
 <212> PRT
 <213> Mus musculus

<400> 35

```

Pro Ser Gln Met Gln Val Thr Asp Val Gln Asp Asn Ser Ile Ser Val
 1              5              10              15

Arg Trp Leu Pro Ser Thr Ser Pro Val Thr Gly Tyr Arg Val Thr Thr
          20              25              30

Thr Pro Lys Asn Gly Leu Gly Pro Ser Lys Thr Lys Thr Ala Ser Pro
          35              40              45

Asp Gln Thr Glu Met Thr Ile Glu Gly Leu Gln Pro Thr Val Glu Tyr
 50              55              60

Val Val Ser Val Tyr Ala Gln Asn Arg Asn Gly Glu Ser Gln Pro Leu
 65              70              75              80

Val Gln Thr Ala Val Thr
          85

```

<210> 36

<211> 87

<212> PRT

<213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: F3-2 repeats from
Unknown WARP

<400> 36

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Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser Leu Arg Val
 1              5              10              15

Ser Trp Ala Pro Ala Leu Gly Pro Asp Ser Ala Leu Gly Tyr His Val
          20              25              30

Gln Leu Gly Pro Leu Gln Gly Gly Ser Leu Glu Arg Val Glu Val Pro
 35              40              45

Ala Gly Gln Asn Ser Thr Thr Val Gln Gly Leu Thr Pro Cys Thr Thr
 50              55              60

Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg Gln Arg Ala
 65              70              75              80

Leu Ser Ala Lys Ala Cys Thr
          85

```

<210> 37

<211> 88

<212> PRT

<213> Homo sapiens

<400> 37

```

Pro Thr Arg Leu Val Phe Ser Ala Leu Gly Pro Thr Ser Leu Arg Val
 1              5              10              15

```

Ser Trp Gln Glu Pro Arg Cys Glu Arg Pro Leu Gln Gly Tyr Ser Val
 20 25 30
 Glu Tyr Gln Leu Leu Asn Gly Gly Glu Leu His Arg Leu Asn Ile Pro
 35 40 45
 Asn Pro Ala Gln Thr Ser Val Val Val Glu Asp Leu Leu Pro Asn His
 50 55 60
 Ser Tyr Val Phe Arg Val Arg Ala Gln Ser Gln Glu Gly Trp Gly Arg
 65 70 75 80
 Glu Arg Glu Gly Val Ile Thr Ile
 85

<210> 38
 <211> 85
 <212> PRT
 <213> Gullus gallus

<400> 38
 Pro Gln His Leu Glu Val Asp Glu Ala Ser Thr Asp Ser Phe Arg Val
 1 5 10 15
 Ser Trp Lys Pro Thr Ser Ser Asp Ile Ala Phe Tyr Arg Leu Ala Trp
 20 25 30
 Ile Pro Leu Asp Gly Gly Glu Ser Glu Glu Val Val Leu Ser Gly Asp
 35 40 45
 Ala Asp Ser Tyr Val Ile Glu Gly Leu Leu Pro Asn Thr Glu Tyr Glu
 50 55 60
 Val Ser Leu Leu Ala Val Phe Asp Asp Glu Thr Glu Ser Glu Val Val
 65 70 75 80
 Ala Val Leu Gly Ala
 85

<210> 39
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 39
 Pro Lys Asp Ile Thr Ile Ser Asn Val Thr Lys Asp Ser Val Met Val
 1 5 10 15
 Ser Trp Ser Pro Pro Val Ala Ser Phe Asp Tyr Tyr Arg Val Ser Tyr
 20 25 30
 Arg Pro Thr Gln Val Gly Arg Leu Asp Ser Ser Val Val Pro Asn Thr
 35 40 45
 Val Thr Glu Phe Thr Ile Thr Arg Leu Asn Pro Ala Thr Glu Tyr Glu
 50 55 60

Ile Ser Leu Asn Ser Val Arg Gly Arg Glu Glu Ser Glu Arg Ile Cys
 65 70 75 80

Thr Leu Val His Thr
 85

<210> 40

<211> 87

<212> PRT

<213> Unknown Sequence

<220>

<223> Description of Unknown Sequence: F3-1 repeat from
 Unknown WARP

<400> 40

Pro Gln Gln Leu His Ala Ser Glu Val Leu Ser Ser Gly Phe Arg Leu
 1 5 10 15

Ser Trp Pro Pro Leu Leu Thr Ala Asp Ser Gly Tyr Tyr Val Leu Glu
 20 25 30

Leu Val Pro Ser Gly Lys Leu Ala Thr Thr Arg Arg Gln Gln Leu Pro
 35 40 45

Gly Asn Ala Thr Ser Trp Thr Trp Thr Asp Leu Asp Pro Asp Thr Asp
 50 55 60

Tyr Glu Val Ser Leu Leu Pro Glu Ser Asn Val His Leu Leu Arg Pro
 65 70 75 80

Gln His Val Arg Val Arg Thr
 85

<210> 41

<211> 2311

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (30)..(1274)

<400> 41

tcgatcaaga gcccgccact ccaggcgcg atg ctg ttc tgg act gcg ttc agc 53
 Met Leu Phe Trp Thr Ala Phe Ser
 1 5

atg gct ttg agt ctg cgg ttg gca ttg gcg cgg agc agc ata gag cgc 101
 Met Ala Leu Ser Leu Arg Leu Ala Leu Ala Arg Ser Ser Ile Glu Arg
 10 15 20

ggt tcc aca gca tca gac ccc cag ggg gac ctg ttg ttc ctg ttg gac 149
 Gly Ser Thr Ala Ser Asp Pro Gln Gly Asp Leu Ser Phe Leu Leu Asp
 25 30 35 40

agc tca gcc agc gtg tca cac tat gag ttc tca aga gtt cgg gaa ttt	197
Ser Ser Ala Ser Val Ser His Tyr Glu Phe Ser Arg Val Arg Glu Phe	
45 50 55	
gtg ggg cag ctg gtg gct acg atg tct ttc gga ccc ggg gct ctg cgt	245
Val Gly Gln Leu Val Ala Thr Met Ser Phe Gly Pro Gly Ala Leu Arg	
60 65 70	
gct agt ctg gtg cac gtg ggc agc cag cct cac aca gag ttt act ttt	293
Ala Ser Leu Val His Val Gly Ser Gln Pro His Thr Glu Phe Thr Phe	
75 80 85	
gac cag tac agt tca ggc cag gct ata cgg gat gcc atc cgt gtt gca	341
Asp Gln Tyr Ser Ser Gly Gln Ala Ile Arg Asp Ala Ile Arg Val Ala	
90 95 100	
ccc caa cgt atg ggt gat acc aac aca ggc ctg gca ctg gct tat gcc	389
Pro Gln Arg Met Gly Asp Thr Asn Thr Gly Leu Ala Leu Ala Tyr Ala	
105 110 115 120	
aaa gaa caa ttg ttt gct gag gaa gca ggt gcc cgg cca ggg gtt ccc	437
Lys Glu Gln Leu Phe Ala Glu Glu Ala Gly Ala Arg Pro Gly Val Pro	
125 130 135	
aag gtg ctg gtg tgg gtg aca gat ggt ggc tcc agc gac ccc gtg ggc	485
Lys Val Leu Val Trp Val Thr Asp Gly Gly Ser Ser Asp Pro Val Gly	
140 145 150	
ccc cct atg cag gag ctc aag gac ctg ggt gtc acc atc ttc att gtc	533
Pro Pro Met Gln Glu Leu Lys Asp Leu Gly Val Thr Ile Phe Ile Val	
155 160 165	
agc act ggc cga ggc aac ctg ttg gag ctg ttg gca gct gcc tcg gct	581
Ser Thr Gly Arg Gly Asn Leu Leu Glu Leu Leu Ala Ala Ser Ala	
170 175 180	
cct gcc gag aag cac cta cac ttt gtg gat gtg gat gat ctt cct atc	629
Pro Ala Glu Lys His Leu His Phe Val Asp Val Asp Asp Leu Pro Ile	
185 190 195 200	
att gcc cgg gag ctg cgg ggc tcc ata act gat gcg atg cag cca caa	677
Ile Ala Arg Glu Leu Arg Gly Ser Ile Thr Asp Ala Met Gln Pro Gln	
205 210 215	
cag ctt cat gcc tcg gag gtt ctg tcc agt ggc ttc cgc ctg tcc tgg	725
Gln Leu His Ala Ser Glu Val Leu Ser Ser Gly Phe Arg Leu Ser Trp	
220 225 230	
ccg ccc ctg ctg aca gcg gac tct ggt tac tac gtg ctg gaa ttg gta	773
Pro Pro Leu Leu Thr Ala Asp Ser Gly Tyr Tyr Val Leu Glu Leu Val	
235 240 245	
cct agc ggc aaa ctg gca acc aca aga cgc caa cag ctg ccc ggg aat	821
Pro Ser Gly Lys Leu Ala Thr Thr Arg Arg Gln Gln Leu Pro Gly Asn	
250 255 260	

gct acc agc tgg acc tgg aca gat ctc gac ccg gac aca gac tat gaa 869
 Ala Thr Ser Trp Thr Trp Thr Asp Leu Asp Pro Asp Thr Asp Tyr Glu
 265 270 275 280

gta tca ctg ctg cct gag tcc aac gtg cac ctc ctg agg ccg cag cac 917
 Val Ser Leu Leu Pro Glu Ser Asn Val His Leu Leu Arg Pro Gln His
 285 290 295

gtg cga gta cgc aca ctg caa gag gag gcc ggg cca gaa cgc atc gtc 965
 Val Arg Val Arg Thr Leu Gln Glu Glu Ala Gly Pro Glu Arg Ile Val
 300 305 310

atc tcg cat gcg agg ccg cgc agc ctc cgc gta agc tgg gcc ccc gcg 1013
 Ile Ser His Ala Arg Pro Arg Ser Leu Arg Val Ser Trp Ala Pro Ala
 315 320 325

ctt ggc ccg gac tcc gct ctc ggc tac cat gta cag ctc gga cct ctg 1061
 Leu Gly Pro Asp Ser Ala Leu Gly Tyr His Val Gln Leu Gly Pro Leu
 330 335 340

cag ggc ggg tcc cta gag cgc gtg gag gtg cca gca ggc cag aac agc 1109
 Gln Gly Gly Ser Leu Glu Arg Val Glu Val Pro Ala Gly Gln Asn Ser
 345 350 355 360

act acc gtc cag ggc ctg acg ccc tgc acc act tac ctg gtg act gtg 1157
 Thr Thr Val Gln Gly Leu Thr Pro Cys Thr Thr Tyr Leu Val Thr Val
 365 370 375

act gcc gcc ttc cgc tcc ggc cgc cag agg gcg ctg tcg gct aag gcc 1205
 Thr Ala Ala Phe Arg Ser Gly Arg Gln Arg Ala Leu Ser Ala Lys Ala
 380 385 390

tgt acg gcc tct ggc gcg cgg acc cgt gct ccg cag tcc atg cgg ccg 1253
 Cys Thr Ala Ser Gly Ala Arg Thr Arg Ala Pro Gln Ser Met Arg Pro
 395 400 405

gag gct gga ccg cgg gag ccc tgaactgcct gcctgctcgt ccaccgggg 1304
 Glu Ala Gly Pro Arg Glu Pro
 410 415

gccctcttcc ctagcccgga gagagagaca ctgctgctcg tgggttttct tgtggatgga 1364

gtcgggtggg gagatgggat gccggtcctg cctttgacca gcgttaattc ctttcgtcgt 1424

ttccccactg gtcacgccc cccttgccctg acttccggga aaccgggta gcctcacgcg 1484

caatggcggg cctctccggg tgccagtgga gttgagcaca cgggtggcct tgggcaactc 1544

ttggcgaggg gatggacagt gtctgaggtc aggttgagga cataagaccc aggaaccgcc 1604

ttcaggagag gaggccacag agtttccaac ctgtgccaaa ggctgggccc tctggtggca 1664

gggactacgc atggctttga ggaggcgttc aggaccatcc aggtcctgcc tgggcctaga 1724

aagtgggtag gagaaaggga agagagacta gtgtagacag gattcccga aacttcctca 1784

aggaaaggaa agataggag gtatgctggg aggtgatga tgtggcattg gttttcatca 1844

agatgtcctg ccagcctaga ggccgggatc tgtcagggtc actgactctg ccttcctgcc 1904
caggacctgc actgggccct cgatcagtgc caaggatgca gtcttttcac aggaatggga 1964
cgagaccttg gcatttaggg cctcagggat aggagagccg cactatgaca gattctaagg 2024
gagcctcctg ctttagtgta gggagcaagg tgtcatgcag gtgggctacc tcctgccatc 2084
accattacc tggggcatct gacagatacc taagggtggt caggaacagg tttcctctca 2144
agtccctatg taggcctctc ctctcctctc agaatcattt gccttatccc aagcttactc 2204
catctcttcc ccactaatga cccggactct aacaacaata cagtcagaca gacataaact 2264
gtgcctgcag tctcattaa atgctgtatt tttcgtcaaa aaaaaaa 2311